

Fig. 1A

1 GCTACCTCCA ACTGCTGAGG AACCGGTTGC CTAAAGGAG CCGCAAAAG
 51 CGCCTACGTG GAGTCCAGAG GAGCGAAGT AGTCAGATT GACTGAGAGC
 101 CGTAAAGCGC GGCTGGCTCT CGTTTCCGG ATAACGACTA CAGCTCCGAC
 151 TGTCAAGTGC GGCCTTCCTC GTGTGAGGG ATCTGCCGA CCCCTGCAAA
 201 TTCAATTCTT TTCCCATTC GGGCCCTTCC CTATCGTCG CCCCTTCACC
 251 TTGGATCATG TTCAAGAAAT TTGATGAAA AGAAAATGTG TCCAACGTCA
 301 TCCAGTTGAA AACTTCAGTT ATTAAGGTA TTAAGAAATCA ATTGATAGAG
 351 CAATTTCAG GTATTGAACC ATGGCTTAAT CAAATCATGC CTAAAGAAAG
 401 TCCTGTCAA ATAGTCCGAT GCCATGAACA TATAGAAATC CTTACAGTAA
 451 ATGGAGAATT ACTCTTTTT AGACAAAGAG AAGGCCCTT TTATCCAACC
 501 CTAAGATTAC TTCACAAATA TCCTTTTATC CTGCCACACC AGCAGGTTGA
 551 TAAAGGAGCC ATCAAATTG TACTCAGTGG AGCAAATATC ATGTGTCCCA
 601 GGCTTAACCT CTCCTGGAGC TAAGCTTTAC CCTGCTGCAG TAGATACCAT
 651 TGTTGCTATC ATGGCAGAAG GAAAACAGCA TGCTCTATGT GTTGGAGTCA
 701 TGAAGATGTC TGCAGAAGAC ATTGAGAAAG TCAACAAAGG AATTGGCATT
 751 GAAAATATCC ATTATTAAA TGATGGGCTG TGGCATATGA AGACATATAA
 801 ATGAGCCTCA GAAGGAATGC ACTTGGGCTA AATATGGATA TTGTGCTGTA
 851 TCTGTGTTG TGTCTGTGTG TGACAGCATG AAGATAATGC CTGTGTTAT
 901 GCTGAATAAA TTCACCAGAT GCTAAAAAAA AAAAAAAA AAAA

Fig. 1B

1 M F K K F D E K E N V S N C I Q L K T S V I K G I K N
 28 Q L I E Q F P G I E P W L N Q I M P K K D P V K I V R
 55 C H E H I E I L T V N G E L L F F R Q R E G P F Y P T
 82 L R L L H K Y P F I L P H Q Q V D K G A I K F V L S G
 109 A N I M C P R L N F S W S

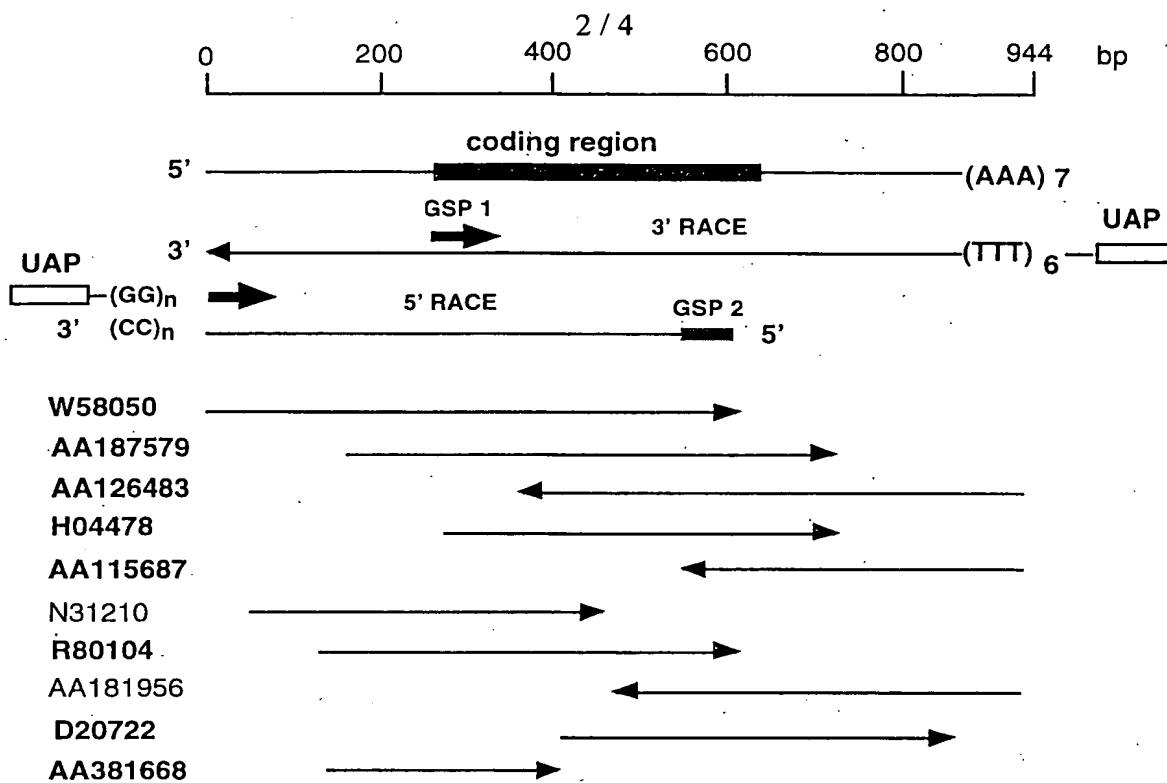


Fig. 2

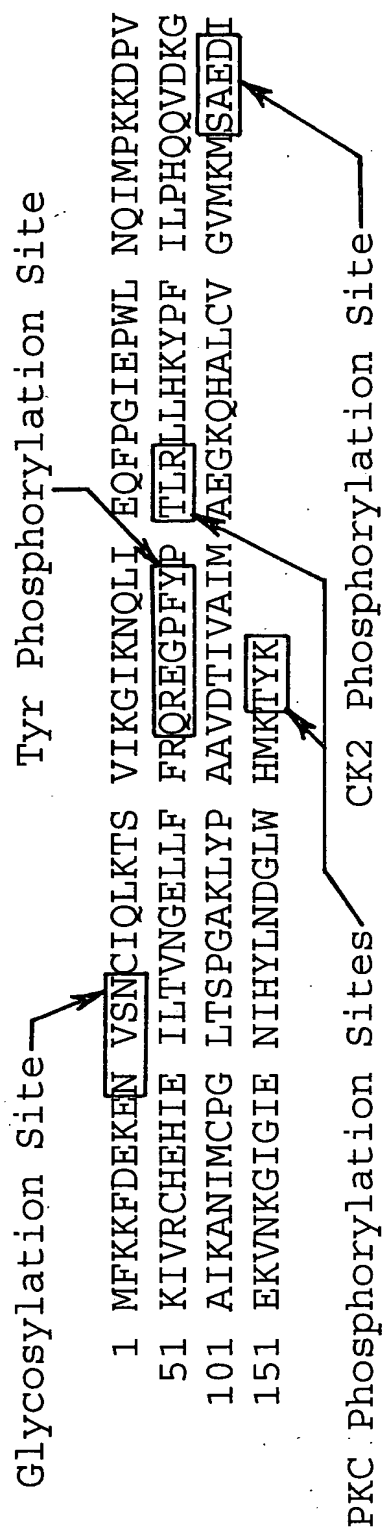


Fig. 3

MCT-1
8 KENVSNCIQLKTSVIKIGIKNQLIEQFPGIEWLNQIMPKDPVK 51
||| | : . | . | : : : | . |
Cyclin H 239 KEN.RTCLSQLLDIMKSMRN.LVKKYE..PPRSEEVAVLKQ..K277

MCT-1 52IVRCHEHIEILTVN 65
Cyclin H 278LERCHS.AE.LALN288

Fig. 4

Fig. 5A

1 GCTACCTCCA ACTGCTGAGG AACCGGTGCG CTAAAGGAG CCGGCAAAAG
51 CGCCTACGTG GAGTCCAGAG GAGCGGAAGT AGTCAGATTG GACTGAGAGC
101 CGTAAAGCGC GGTGGCTCT CGTTTCCGG ATAACGACTA CAGCTCCGAC
151 TGTCAGTGCC GGCCTTCCCTC GTGTGAGGG ATCTGCCGGA CCCCTGCAAA
201 TTCAATTCT TTTCCATTCC GGGCCCTTCC CTATCGTCGC CCCCTTCACC
251 TTGGATC**ATG** TTCAAGAAAT TTGATGAAAA AGAAAATGTG TCCAACTGCA
301 TCCAGTTGAA AACTTCAGTT ATTAAGGTA TTAAGAAATCA ATTGATAGAG
351 CAATTTCCAG GTATTGAACC ATGGCTTAAT CAAATCATGC CTAAGAAAGA
401 TCCTGTCAAA ATAGTCCGAT GCCATGAACA TATAGAAATC CTTACAGTAA
451 ATGGAGAATT ACTCTTTTTC AGACAAAGAG AAGGGCCTTT TTATCCAAACC
501 CTAAGATTAC TTCACAAATA TCCTTTTATC CTGCCACACC AGCAGGTTGA
551 TAAAGGAGCC ATCAAATTG TACTCAGTG AGCAAATATC ATGTGTCCAG
601 GCTTAACTC TCCTGGAGCT AAGCTTTACC CTGCTGCAGT AGATACCATT
651 GTTGCTATCA TGGCAGAAGG AAAACAGCAT GCTCTATGTG TTGGAGTCAT
701 GAAGATGTCT GCAGAAGACA TTGAGAAAGT CAACAAAGGA ATTGGCATTG
751 AAAATATCCA TTATTTAAAT GATGGGCTGT GGCATATGAA GACATATAAA
801 **TGAG**CCCTCAG AAGGAATGCA CTGGGGCTAA ATATGGATAT TGTGCTGTAT
851 CTGTGTTTGT GTCTGTGTGT GACAGCATGA AGATAATGCC TGTGGTTATG
901 CTGAATAAAAT TCACCAGATG CTAAAAAAA AAAA

Fig. 5B

1 M F K K F D E K E N V S N C I Q L K T S V I K G I K N
28 Q L I E Q F P G I E P W L N Q I M P K K D P V K I V R
55 C H E H I E I L T V N G E L L F F R Q R E G P F Y P T
82 L R L L H K Y P F I L P H Q Q V D K G A I K F V L S G
109 A N I M C P G L T S P G A K L Y P A A V D T I V A I M
136 A E G K Q H A L C V G V M K M S A E D I E K V N K G I
163 G I E N I H Y L L N D G L W H M K T Y K